



Patent Docket P0897C2

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Goeddel, David V.  
Rothe, Mike

(ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

(iii) NUMBER OF SEQUENCES: 59

#### (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

#### (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

#### (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE: 07-Jan-1997  
(C) CLASSIFICATION:

#### (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dreger, Ginger R.  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: P0897C2

#### (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-3216  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

### (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2088 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50  
GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100  
GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150  
CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200  
ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250  
GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300  
GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350  
ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400  
GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450  
TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500  
GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550  
CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600  
CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650  
AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700  
CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750  
GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

ACATTGTTGC TGTCTCAAC AAGGAAGTGG AGGCTTCCA CCTGGCACTG 850  
GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900  
GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950  
TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000  
GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050  
GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100  
CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150  
TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200  
ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250  
TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300  
CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350  
CGGCTGCCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCAAGCACG 1400  
CCTACGTCAA AGATGACACA ATGTTCTCA AATGCATTGT GGACACTAGT 1450  
GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500  
GGGGACTION TAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCACAGCC 1550  
CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTAGCGCC ACAGCATGCT 1600  
GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650  
GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700  
GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750  
GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800  
AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850

TGGA AAAATG CCCCCATCTC TCTG TTCAGA CTC AAAACTA GAACCACAGG 1900  
GCAGAAGGGT CAGACATTAA TGTGAATT TA ACCTGCCCTG GACTGAGTTC 1950  
CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000  
TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050  
ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAAAA 2088

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Ser	Ser	Ala	Pro	Asp	Glu	Asn	Glu	Phe	Gln	Phe	Gly
1		5			10			15						
Cys	Pro	Pro	Ala	Pro	Cys	Gln	Asp	Pro	Ser	Glu	Pro	Arg	Val	Leu
		20			25			30						
Cys	Cys	Thr	Ala	Cys	Leu	Ser	Glu	Asn	Leu	Arg	Asp	Asp	Glu	Asp
		35			40			45						
Arg	Ile	Cys	Pro	Lys	Cys	Arg	Ala	Asp	Asn	Leu	His	Pro	Val	Ser
		50			55			60						
Pro	Gly	Ser	Pro	Leu	Thr	Gln	Glu	Lys	Val	His	Ser	Asp	Val	Ala
		65			70			75						
Glu	Ala	Glu	Ile	Met	Cys	Pro	Phe	Ala	Gly	Val	Gly	Cys	Ser	Phe
		80			85			90						
Lys	Gly	Ser	Pro	Gln	Ser	Met	Gln	Glu	His	Glu	Ala	Thr	Ser	Gln
		95			100			105						

Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys  
110 115 120

Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu  
125 130 135

Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr  
140 145 150

Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser  
155 160 165

Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu  
170 175 180

Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala  
185 190 195

Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala  
200 205 210

Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu  
215 220 225

Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp  
230 235 240

Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu  
245 250 255

Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr  
260 265 270

Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe  
275 280 285

Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu  
290 295 300

Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu  
305 310 315

Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu  
320 325 330

Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln  
335 340 345

Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser  
350 355 360

Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser  
365 370 375

Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys  
380 385 390

His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val  
395 400 405

Asp Thr Ser Ala  
409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2121 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50  
GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100  
CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150  
CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200  
CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250

115

CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300  
TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCCGAG AGAGGTGGAG 350  
AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400  
GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTCTGCTGACGG 450  
AGTGTCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500  
ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550  
ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600  
TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650  
TTTCAGGACC ATGTTAGAGC ATGCAGCAA TGCCGGGTTC TCTGCAGATT 700  
CCACACCGTT GGCTGTTTCA AGATGGTGGA GACTGAGAAC CTGCAGGATC 750  
ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800  
TTGGAGGCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850  
ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900  
TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950  
GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000  
TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050  
TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100  
GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150  
CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200  
GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250  
GGGCGGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300

116

TGATGCTCTG TTGCAGTGGC CTTTAAATCA GAAGGTAACA TTGATGTTGC 1350  
TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400  
ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450  
CTGCCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500  
TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550  
TAGCCACCCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600  
CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650  
GGAGGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700  
AGCCTCCAGT TGGCCTTCAG CTGGCAAACCT GAGTTGGACG GTCCACTGAG 1750  
CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800  
AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGAC CTGTAGGTGG 1850  
GTGCTCAGAA AGGGCCTCTC CAGAGAGAGT CTCAAGAGCT GCAGCAGGAG 1900  
CAAAGTGACT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950  
ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000  
CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050  
TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100  
CGACAAAAAA AAAAAAAAAA A 2121

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Ala	Ala	Ser	Val	Thr	Ser	Pro	Gly	Ser	Leu	Glu	Leu	Leu
1		5			10				15					
Gln	Pro	Gly	Phe	Ser	Lys	Thr	Leu	Leu	Gly	Thr	Arg	Leu	Glu	Ala
		20			25				30					
Lys	Tyr	Leu	Cys	Ser	Ala	Cys	Lys	Asn	Ile	Leu	Arg	Arg	Pro	Phe
		35			40				45					
Gln	Ala	Gln	Cys	Gly	His	Arg	Tyr	Cys	Ser	Phe	Cys	Leu	Thr	Ser
		50			55				60					
Ile	Leu	Ser	Ser	Gly	Pro	Gln	Asn	Cys	Ala	Ala	Cys	Val	Tyr	Glu
		65			70				75					
Gly	Leu	Tyr	Glu	Glu	Gly	Ile	Ser	Ile	Leu	Glu	Ser	Ser	Ser	Ala
		80			85				90					
Phe	Pro	Asp	Asn	Ala	Ala	Arg	Arg	Glu	Val	Glu	Ser	Leu	Pro	Ala
		95			100				105					
Val	Cys	Pro	Asn	Asp	Gly	Cys	Thr	Trp	Lys	Gly	Thr	Leu	Lys	Glu
		110			115				120					
Tyr	Glu	Ser	Cys	His	Glu	Gly	Leu	Cys	Pro	Phe	Leu	Leu	Thr	Glu
		125			130				135					
Cys	Pro	Ala	Cys	Lys	Gly	Leu	Val	Arg	Leu	Ser	Glu	Lys	Glu	His
		140			145				150					
His	Thr	Glu	Gln	Glu	Cys	Pro	Lys	Arg	Ser	Leu	Ser	Cys	Gln	His
		155			160				165					
Cys	Arg	Ala	Pro	Cys	Ser	His	Val	Asp	Leu	Glu	Val	His	Tyr	Glu
		170			175				180					
Val	Cys	Pro	Lys	Phe	Pro	Leu	Thr	Cys	Asp	Gly	Cys	Gly	Lys	Lys
		185			190				195					

Lys Ile Pro Arg Glu Thr Phe Gln Asp His Val Arg Ala Cys Ser  
200 205 210

Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu  
215 220 225

Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu  
230 235 240

Arg Glu His Leu Ala Leu Leu Leu Ser Ser Phe Leu Glu Ala Gln  
245 250 255

Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln  
260 265 270

Arg Cys Gln Ile Leu Glu Gln Lys Ile Ala Thr Phe Glu Asn Ile  
275 280 285

Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala  
290 295 300

Glu Ala Cys Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu  
305 310 315

Ala Leu Ser Asn Lys Val Gln Gln Leu Glu Arg Ser Ile Gly Leu  
320 325 330

Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys Val Ser Glu Leu  
335 340 345

Glu Val Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys Ile Ser Asp  
350 355 360

Phe Thr Arg Lys Arg Gln Glu Ala Val Ala Gly Arg Thr Pro Ala  
365 370 375

Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys Met  
380 385 390

Cys Leu Arg Val Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr  
395 400 405

His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala  
 410 415 420

Leu Leu Gln Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu  
 425 430 435

Asp His Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp  
 440 445 450

Val Thr Ser Ser Ser Phe Gln Arg Pro Val Ser Asp Met Asn Ile  
 455 460 465

Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala  
 470 475 480

Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile  
 485 490 495

Val Asp Leu Thr Gly Leu  
 500 501

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe  
 1 5 10 15

Leu Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr  
 20 25 30

His Leu Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His  
 35 40 44

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Ser Cys Ser Ile Cys Leu Glu Pro Phe Lys Glu Pro Val  
1 5 10 15

Thr Thr Pro Cys Gly His Asn Phe Cys Gly Ser Cys Leu Asn Glu  
20 25 30

Thr Trp Ala Val Gln Gly Ser Pro Tyr Leu Cys Pro Gln Cys Arg  
35 40 45

Ala Val  
47

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Leu Arg Cys His Ile Cys Lys Asp Phe Leu Lys Val Pro Val  
1 5 10 15

Leu Thr Pro Cys Gly His Thr Phe Cys Ser Leu Cys Ile Arg Thr  
20 25 30

His Leu Asn Asn Gln Pro Asn Cys Pro Leu Cys Leu Phe Glu  
35 40 44

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met  
1 5 10 15

Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg  
20 25 30

Cys Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr  
35 40 44

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val  
1 5 10 15

Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg  
20 25 30

Cys Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:



Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val  
1 5 10 15

Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln  
20 25 30

Val Gly Lys Gly Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg  
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met  
1 5 10 15

Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val  
20 25 30

Thr Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys  
35 40 45

Lys  
46

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val  
1 5 10 15

Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu  
20 25 30

Asn Tyr Glu Ser Asn Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro  
35 40 45

Val Cys Arg Val Pro  
50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met  
1 5 10 15

Met Leu Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg  
20 25 30

Cys Trp Gly Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg  
35 40 45

Glu Thr  
47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Gln Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys  
1 5 10 15

Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser  
20 25 30

Trp Gln Glu Ser Glu Gly Gln Gly Ser Ser Gly Cys Pro Phe Cys  
35 40 45

Arg Cys Glu  
48

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Phe Lys Leu Val Thr Cys Asp Phe Cys Lys Arg Asp Asp  
1 5 10 15

Ile Lys Lys Lys Glu Leu Glu Thr His Tyr Lys Thr Cys  
20 25 28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Asp Leu Ala Val Cys Asp Val Cys Asn Arg Lys Phe Arg His  
1 5 10 15

Lys Asp Tyr Leu Arg Asp His Gln Lys Thr His  
20 25 26

(2) INFORMATION FOR SEQ ID NO:17:

125



(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gly Lys Tyr Pro Phe Ile Cys Ser Glu Cys Gly Lys Ser Phe  
1            5            10            15

Met Asp Lys Arg Tyr Leu Lys Ile His Ser Asn Val His  
          20            25            28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Glu Lys Pro Tyr Thr Cys Thr Val Cys Gly Lys Lys Phe  
1            5            10            15

Ile Asp Arg Ser Ser Val Val Lys His Ser Arg Thr His  
          20            25            28

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Lys Lys Phe Pro His Ile Cys Gly Glu Cys Gly Lys Gly Phe  
1            5            10            15

Arg His Pro Ser Ala Leu Lys Lys His Ile Arg Val His  
20 25 28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Glu Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly Lys Lys Phe  
1 5 10 15

Arg Thr Ala Arg His Leu Val Lys His Gln Arg Ile His  
20 25 28

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Pro Asn Glu Gln Met Ala Gln Cys Pro Ile Cys Gln Gln Phe Tyr  
1 5 10 15

Pro Leu Lys Ala Leu Glu Lys Thr His Leu Asp Glu Cys  
20 25 28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Asp Asp Gly Leu Val Ala Cys Pro Ile Cys Leu Thr Arg Met  
1 5 10 15

Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys  
20 25 28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTTGTGCCT GCAGAGAGAA G 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGGTTAAC TTTCGGTGCT CCCCAGCAGG GTCTC 35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

128

CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGGTTAAC TGCACTGGCC GAGCTCTCCA GGGA 34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGATGAGAA TTCAT 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATGAATTC TCATCACTGC A 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCTGGTTAA CTGGGC 16

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCNCCNATGG CNYTNGARC 19

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCNCCNATGG CNYTNGARA 19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCCNATGG CNYTNGARG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AARCAYGCNT AYGTNAA 17

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTNACRTANG CRTGYTT 17

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:



Ala Pro Met Ala Leu Glu Arg

1            5       7

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys His Ala Tyr Val Lys

1            5       6

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Pro Gly Ser Asn Leu Gly Ser

1            5       7

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Lys Asp Asp Thr Met Phe Leu Lys

1            5            8

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGGATCC GGAGACACAG ATTCCAGCCC C 31

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGAATTC TTA ACTCTTC GGTGCTCCCC AGCAG 35

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGGCTGGC CTAATGT 17

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCTGGCGAA GAAGTCC 17

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 31

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Goeddel, David V.  
Rothe, Mike
- (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
- 10 (iii) NUMBER OF SEQUENCES: 62
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
15 (C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080
- 20 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: patin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 27-May-1994  
30 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- 35 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Dreger, Ginger R.  
(B) REGISTRATION NUMBER: 33,055  
(C) REFERENCE/DOCKET NUMBER: 897
- 40 (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 415/225-3216  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168
- 45 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2088 bases

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCAGCCCCG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50

10 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100

15 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150

CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200

20 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250

GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC 300

25 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350

30 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400

GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450

35 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500

GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC 550

40 CTGTACCTGC TGCTGGCGGT CTAAAGGAG TGGAAATCCT CACCAGGCTC 600

45 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650

AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700



CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750

5 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800

ACATTGTTGC TGTCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850

10 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900

GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950

15 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000

20 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050

GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100

25 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150

TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200

30 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250

35 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300

CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350

40 CGGCTGCCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCAAGCACG 1400

CCTACGTCAA AGATGACACA ATGTTCTCA AATGCATTGT GGACACTAGT 1450

45 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500

GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550

CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTGAGCGCC ACAGCATGCT 1600

GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650

GGAGGAGAAG ACAGAAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700

GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750

GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800

AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850

TGGAAAAATG CCCCCATCTC TCTGTTTCTG CTCAAACTA GAACCACAGG 1900

GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950

CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAACTG CCCTGGGAAA 2000

TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050

ATAACAAAAG CTTGAATTG CAAAAAAAAA AAAAAAAAAA 2088

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Ser	Ser	Ala	Pro	Asp	Glu	Asn	Glu	Phe	Gln	Phe	Gly
1			5			10				15				

	Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu	
	20                      25                      30	
5	Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp	
	35                      40                      45	
	Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser	
	50                      55                      60	
10	Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala	
	65                      70                      75	
	Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe	
	80                      85                      90	
15	Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln	
	95                      100                      105	
	Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys	
20	110                      115                      120	
	Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu	
	125                      130                      135	
25	Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr	
	140                      145                      150	
	Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser	
	155                      160                      165	
30	Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu	
	170                      175                      180	
	Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala	
35	185                      190                      195	
	Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala	
	200                      205                      210	
40	Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu	
	215                      220                      225	
	Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp	
	230                      235                      240	
45	Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu	
	245                      250                      255	

Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr  
260 265 270

Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe  
275 280 285

Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu  
290 295 300

Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu  
305 310 315

Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu  
320 325 330

Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln  
335 340 345

Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser  
350 355 360

Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser  
365 370 375

Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys  
380 385 390

His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val  
395 400 405

Asp Thr Ser Ala  
409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2121 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG 50

GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG 100

CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT 150

5 CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC 200

CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA 250

10 CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT 300

TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCCGAG AGAGGTGGAG 350

15 AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT 400

GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG 450

AGTGCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC 500

25 ACTGAGCAGG AATGCCCCAA AAGGAGCCTG AGCTGCCAGC ACTGCAGAGC 550

ACCCTGTAGC CACGTGGACC TGGAGGTACA CTATGAGGTC TGCCCCAAGT 600

30 TTCCCTTAAC CTGTGATGGC TGTGGCAAGA AGAAGATCCC TCGGGAGACG 650

TTTCAGGACC ATGTTAGAGC ATGCAGCAA TGCCGGGTTC TCTGCAGATT 700

CCACACCGTT GGCTGTTCAG AGATGGTGGA GACTGAGAAC CTGCAGGATC 750

40 ATGAGCTGCA GCGGCTACGG GAACACCTAG CCCTACTGCT GAGCTCATTC 800

TTGGAGGCCC AAGCCTCTCC AGGAACCTTG AACCAGGTGG GGCCAGAGCT 850

45 ACTCCAGCGG TGCCAGATTT TGGAGCAGAA GATAGCAACC TTTGAGAACA 900

TTGTCTGCGT CTTGAACCGT GAAGTAGAGA GGGTAGCAGT GACTGCAGAG 950

5 GCTTGTAGCC GGCAGCACCG GCTAGACCAG GACAAGATTG AGGCCCTGAG 1000

TAACAAGGTG CAACAGCTGG AGAGGAGCAT CGGCCTCAAG GACCTGGCCA 1050

10 TGGCTGACCT GGAGCAGAAG GTCTCCGAGT TGGAAGTATC CACCTATGAT 1100

GGGGTCTTCA TCTGGAAGAT CTCTGACTTC ACCAGAAAGC GTCAGGAAGC 1150

15 CGTAGCTGGC CGGACACCAG CTATCTTCTC CCCAGCCTTC TACACAAGCA 1200

20 GATATGGCTA CAAGATGTGT CTACGAGTCT ACTTGAATGG CGACGGCACT 1250

GGGCGGGGAA CTCATCTGTC TCTCTTCTTC GTGGTGATGA AAGGCCCCAA 1300

25 TGATGCTCTG TTGCAGTGGC CTTTAAATCA GAAGGTAACA TTGATGTTGC 1350

TGGACCATAA CAACCGGGAG CATGTGATCG ACGCATTCAG GCCCGATGTA 1400

30 ACCTCGTCCT CCTTCCAGAG GCCTGTCAGT GACATGAACA TCGCCAGTGG 1450

35 CTGCCCCCTC TTCTGCCCTG TGTCCAAGAT GGAGGCCAAG AATTCCTATG 1500

TGCGGGATGA TGCGATCTTC ATCAAAGCTA TTGTGGACCT AACAGGACTC 1550

40 TAGCCACCCC TGCTAAGAAT AGCAGCTCAG TGAGGAGCTG TCACATTAGG 1600

CCAGCCAGGC CCTGCCACAC ACGGGTGGGC AGGCTTGGTG TAAATGCTGG 1650

45 GGAGGGCCTC AGCCTAGAGC CAATCACCAT CACACAGAAA GGCAGGAAGA 1700

AGCCTCCAGT TGGCCTTCAG CTGGCAAAC T GAGTTGGACG GTCCACTGAG 1750

CTCAAGGGCC TGGTGGAGCC CGCTGGGGAG CTTCTCAGCT TTCCAATAGG 1800

AAAGCTCCTG CTGTCTCCTC TGTCTGGGGA AGGGAGAGAC CTGTAGGTGG 1850

GTGCTCAGAA AGGGCCTCTC CAGAGAGAGT CTCAAGAGCT GCAGCAGGAG 1900

CAAAGTGA CT GGCCTTCCCC ACCCCATCCT TTGGAAAAGA GGTAGCGGCT 1950

ACACAGGAGA AGGCATGCGC CTGCAGGGTG TAGCCCAAGA GAGAAGCTCT 2000

CTGAGACATA GGCCCTCACT GGAGAAGGGC CTGCCTGGGC TGCACAGCCT 2050

TGCCAGGTGG CCTGTATGGG GGAGAAGTGA TTAAATGTTG AGATGTCACA 2100

CGACAAAAAA AAAAAAAAAA A 2121

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ala Ala Ser Val Thr Ser Pro Gly Ser Leu Glu Leu Leu  
1 5 10 15

Gln Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Arg Leu Glu Ala  
20 25 30

Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe  
35 40 45

Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser  
50 55 60

	Ile Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu	
	65	70 75
5	Gly Leu Tyr Glu Glu Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala	
	80	85 90
	Phe Pro Asp Asn Ala Ala Arg Arg Glu Val Glu Ser Leu Pro Ala	
	95	100 105
10	Val Cys Pro Asn Asp Gly Cys Thr Trp Lys Gly Thr Leu Lys Glu	
	110	115 120
	Tyr Glu Ser Cys His Glu Gly Leu Cys Pro Phe Leu Leu Thr Glu	
	125	130 135
15	Cys Pro Ala Cys Lys Gly Leu Val Arg Leu Ser Glu Lys Glu His	
	140	145 150
	His Thr Glu Gln Glu Cys Pro Lys Arg Ser Leu Ser Cys Gln His	
20	155	160 165
	Cys Arg Ala Pro Cys Ser His Val Asp Leu Glu Val His Tyr Glu	
	170	175 180
25	Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys Gly Lys Lys	
	185	190 195
	Lys Ile Pro Arg Glu Thr Phe Gln Asp His Val Arg Ala Cys Ser	
	200	205 210
30	Lys Cys Arg Val Leu Cys Arg Phe His Thr Val Gly Cys Ser Glu	
	215	220 225
	Met Val Glu Thr Glu Asn Leu Gln Asp His Glu Leu Gln Arg Leu	
35	230	235 240
	Arg Glu His Leu Ala Leu Leu Leu Ser Ser Phe Leu Glu Ala Gln	
	245	250 255
40	Ala Ser Pro Gly Thr Leu Asn Gln Val Gly Pro Glu Leu Leu Gln	
	260	265 270
	Arg Cys Gln Ile Leu Glu Gln Lys Ile Ala Thr Phe Glu Asn Ile	
	275	280 285
45	Val Cys Val Leu Asn Arg Glu Val Glu Arg Val Ala Val Thr Ala	
	290	295 300



	Glu Ala Cys Ser Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu	
	305 310 315	
5	Ala Leu Ser Asn Lys Val Gln Gln Leu Glu Arg Ser Ile Gly Leu	
	320 325 330	
	Lys Asp Leu Ala Met Ala Asp Leu Glu Gln Lys Val Ser Glu Leu	
	335 340 345	
10	Glu Val Ser Thr Tyr Asp Gly Val Phe Ile Trp Lys Ile Ser Asp	
	350 355 360	
	Phe Thr Arg Lys Arg Gln Glu Ala Val Ala Gly Arg Thr Pro Ala	
15	365 370 375	
	Ile Phe Ser Pro Ala Phe Tyr Thr Ser Arg Tyr Gly Tyr Lys Met	
	380 385 390	
20	Cys Leu Arg Val Tyr Leu Asn Gly Asp Gly Thr Gly Arg Gly Thr	
	395 400 405	
	His Leu Ser Leu Phe Phe Val Val Met Lys Gly Pro Asn Asp Ala	
	410 415 420	
25	Leu Leu Gln Trp Pro Phe Asn Gln Lys Val Thr Leu Met Leu Leu	
	425 430 435	
	Asp His Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg Pro Asp	
30	440 445 450	
	Val Thr Ser Ser Ser Phe Gln Arg Pro Val Ser Asp Met Asn Ile	
	455 460 465	
35	Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala	
	470 475 480	
	Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile	
	485 490 495	
40	Val Asp Leu Thr Gly Leu	
	500 501	

(2) INFORMATION FOR SEQ ID NO:5:

45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 44 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Leu Cys Pro Ile Cys Met Gln Ile Ile Lys Asp Ala Phe  
 1 5 10 15

Leu Thr Ala Cys Gly His Ser Phe Cys Tyr Met Cys Ile Ile Thr  
 20 25 30

His Leu Arg Asn Lys Ser Asp Cys Pro Cys Cys Ser Gln His  
 35 40 44

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Ser Cys Ser Ile Cys Leu Glu Pro Phe Lys Glu Pro Val  
 1 5 10 15

Thr Thr Pro Cys Gly His Asn Phe Cys Gly Ser Cys Leu Asn Glu  
 20 25 30

Thr Trp Ala Val Gln Gly Ser Pro Tyr Leu Cys Pro Gln Cys Arg  
 35 40 45

Ala Val  
 47

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Leu Arg Cys His Ile Cys Lys Asp Phe Leu Lys Val Pro Val  
 1 5 10 15

Leu Thr Pro Cys Gly His Thr Phe Cys Ser Leu Cys Ile Arg Thr  
 20 25 30

His Leu Asn Asn Gln Pro Asn Cys Pro Leu Cys Leu Phe Glu

35

40

44

## (2) INFORMATION FOR SEQ ID NO:8:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met  
 1 5 10 15

15

Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg  
 20 25 30

20

Cys Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr  
 35 40 44

## (2) INFORMATION FOR SEQ ID NO:9:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30

Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val  
 1 5 10 15

35

Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg  
 20 25 30

Cys Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro  
 35 40 45

40

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val  
 1 5 10 15

Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln  
 20 25 30

Val Gly Lys Gly Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met  
 1 5 10 15

Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val  
 20 25 30

Thr Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys  
 35 40 45

Lys  
 46

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val  
 1 5 10 15

Ser Ala Asp Cys Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu  
 20 25 30

Asn Tyr Glu Ser Asn Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro  
 35 40 45

Val Cys Arg Val Pro  
50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met  
1 5 10 15

Met Leu Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg  
20 25 30

Cys Trp Gly Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg  
35 40 45

Glu Thr  
47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Gln Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys  
1 5 10 15

Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser  
20 25 30

Trp Gln Glu Ser Glu Gly Gln Gly Ser Ser Gly Cys Pro Phe Cys  
35 40 45

Arg Cys Glu  
48

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Phe Lys Leu Val Thr Cys Asp Phe Cys Lys Arg Asp Asp  
1 5 10 15

10 Ile Lys Lys Lys Glu Leu Glu Thr His Tyr Lys Thr Cys  
20 25 28

(2) INFORMATION FOR SEQ ID NO:16:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Asp Leu Ala Val Cys Asp Val Cys Asn Arg Lys Phe Arg His  
1 5 10 15

25 Lys Asp Tyr Leu Arg Asp His Gln Lys Thr His  
20 25 26

(2) INFORMATION FOR SEQ ID NO:17:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gly Lys Tyr Pro Phe Ile Cys Ser Glu Cys Gly Lys Ser Phe  
1 5 10 15

40 Met Asp Lys Arg Tyr Leu Lys Ile His Ser Asn Val His  
20 25 28

(2) INFORMATION FOR SEQ ID NO:18:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Glu Lys Pro Tyr Thr Cys Thr Val Cys Gly Lys Lys Phe  
 1 5 10 15

Ile Asp Arg Ser Ser Val Val Lys His Ser Arg Thr His  
 20 25 28

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Lys Lys Phe Pro His Ile Cys Gly Glu Cys Gly Lys Gly Phe  
 1 5 10 15

Arg His Pro Ser Ala Leu Lys Lys His Ile Arg Val His  
 20 25 28

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Glu Glu Lys Pro Phe Glu Cys Glu Glu Cys Gly Lys Lys Phe  
 1 5 10 15

Arg Thr Ala Arg His Leu Val Lys His Gln Arg Ile His  
 20 25 28

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Pro Asn Glu Gln Met Ala Gln Cys Pro Ile Cys Gln Gln Phe Tyr

1            5            10            15

Pro Leu Lys Ala Leu Glu Lys Thr His Leu Asp Glu Cys  
                 20                   25                   28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Asp Asp Gly Leu Val Ala Cys Pro Ile Cys Leu Thr Arg Met  
1            5            10            15

Lys Glu Gln Gln Val Asp Arg His Leu Asp Thr Ser Cys  
                 20                   25                   28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTTGTGCCT GCAGAGAGAA G 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGGTTAAC TTTCGGTGCT CCCAGCAGG GTCTC 35



(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTAGGTTAAC TGGAGAAGGG GACCTGCTCG TCCTT 35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTAGGTTAAC TGCTGGCTTG GGAGGAGCAC TGTGA 35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGGTTAAC TGCTCCCGGT GCTGGCCCGG GCCTC 35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGGTAAAC TGCACTGGCC GAGCTCTCCA GGGA 34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGATGAGAA TTCAT 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATGAATTC TCATCACTGC A 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5

GATCGGATCC AAAAAGAAGC CCTTGTGCCT GCA 33

10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 16 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

20

GCCTGGTTAA CTGGGC 16

25

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 19 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

35

GCNCCNATGG CNYTNGARC 19

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCNCCNATGG CNYTNGARA 19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCCNATGG CNYTNGARG 19

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GYTCNARNGC CATNGGNGC 19

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TYTCNARNGC CATNGGNGC 19

5 (2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

15

CYTCNARNGC CATNGGNGC 19

20 (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30

AARCAYGCNT AYGTNAA 17

35 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

45

TTNACRTANG CRTGYTT 17

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Ser Asn Leu Gly Ser  
1 5 7

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys Asp Asp Thr Met Phe Leu Lys  
1 5 8

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Pro Gly Ser Asn Leu Gly Ser  
1 5 7

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Lys Asp Asp Thr Met Phe Leu Lys  
1 5 8

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAGATCT GTTAACTTTC GGTGCTCCCC AGCAGGGTCT C 41

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGAGATCT GTTAACTGGA GAAGGGGACC TGCTCGTCCT T 41

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAGATCT GTTAACTGCT GGCTTGGGAG GAGCACTGTG A 41

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCGATCGTCG ACCAAAAAGA AGCCCTCCTG CCTACAA 37

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAGAGATCT CAGGGGTCAG GCCACTTT 28

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCGATCGTCG ACCGCCTCCA GCTCAGCCCC TGAT 34

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATCGGATCC GGAGACACAG ATTCCAGCCC C 31

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGAATTC TTA ACTCTTC GGTGCTCCCC AGCAG 35

5

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

15

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

30

CCTGGCTGGC CTAATGT 17

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 60 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

45

GATCGACTCG AGATGCCCAA GAAGAAGCGG AAGGTGGCTG CAGCCAGTGT 50

GACTTCCCCT 60

5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 bases

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

15

CTCTGGCGAA GAAGTCC 17

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30

GATCGGATCC GCCTCCAGCT CAGCCCCTGA T 31

35

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

45

GATCGGATCC AGCCAGCAGC TTCTCCTTCA C 31

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCGGATCC TTGTGGTGTG TGGGGGTTGT 30

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCGGATCC GCTCAGGCTC TTTTGGGGCA 30